California Institute for Regenerative Medicine

Temporal and spatial variation of the human microbiota during pregnancy.

Public Summary:

Despite the critical role of the human microbiota in health, our understanding of microbiota compositional dynamics during and after pregnancy is incomplete. We conducted a case-control study of 49 pregnant women, 15 of whom delivered preterm. From 40 of these women, we analyzed bacterial taxonomic composition of 3,767 specimens collected prospectively and weekly during gestation and monthly after delivery from the vagina, distal gut, saliva, and tooth/gum. Linear mixed-effects modeling, medoid-based clustering, and Markov chain modeling were used to analyze community temporal trends, community structure, and vaginal community state transitions. Microbiota community taxonomic composition and diversity remained remarkably stable at all four body sites during pregnancy (P > 0.05 for trends over time). Prevalence of a Lactobacillus-poor vaginal community state type (CST 4) was inversely correlated with gestational age at delivery (P = 0.0039). Risk for preterm birth was more pronounced for subjects with CST 4 accompanied by elevated Gardnerella or Ureaplasma abundances. This finding was validated with a set of 246 vaginal specimens from nine women (four of whom delivered preterm). Most women experienced a postdelivery disturbance in the vaginal community characterized by a decrease in Lactobacillus species and an increase in diverse anaerobes such as Peptoniphilus, Prevotella, and Anaerococcus species. This disturbance was unrelated to gestational age at delivery and persisted for up to 1 y. These findings have important implications for predicting premature labor, a major global health problem, and for understanding the potential impact of a persistent, altered postpartum microbiota on maternal health, including outcomes of pregnancies following short interpregnancy intervals.

Scientific Abstract:

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